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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/812,283

DATE: 07/30/2001
TIME: 12:09:15

Input Set : N:\Crf3\RULE60\09812283.txt
Output Set: N:\CRF3\07302001\I812283.raw

ENTERED

<110> APPLICANT: Fischer, Robert L.
Ohad, Nir
Kiyosue, Tomohiro
Yadegari, Ramin
Margossian, Linda
Harada, John
Goldberg, Robert B.
The Regents of the University of California
<120> TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit Development in Plants
<130> FILE REFERENCE: 023070-086120US
<140> CURRENT APPLICATION NUMBER: 09/812,283
<141> CURRENT FILING DATE: 2001-03-19
<150> PRIOR APPLICATION NUMBER: 09/177,249
<151> PRIOR FILING DATE: 1998-10-22
<150> PRIOR APPLICATION NUMBER: US 09/071,838
<151> PRIOR FILING DATE: 1998-05-01
<160> NUMBER OF SEQ ID NOS: 324
<170> SOFTWARE: PatentIn Ver. 2.0
<210> SEQ ID NO: 1
<211> LENGTH: 2136
<212> TYPE: DNA
<213> ORGANISM: Arabidopsis sp.
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (43)..(2112)
<223> OTHER INFORMATION: fertilization-independent endosperm 1 (FIE1) cDNA
<400> SEQUENCE: 1

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                                              Met Glu Lys Glu
                                                1

aac cat gag gac gat ggt gag ggt ttg cca ccc gaa cta aat cag ata   102
Asn His Glu Asp Asp Gly Glu Gly Leu Pro Pro Glu Leu Asn Gln Ile
  5                  10                  15                  20

aaa gag caa atc gaa aag gag aga ttt ctg cat atc aag aga aaa ttc   150
Lys Glu Gln Ile Glu Lys Glu Arg Phe Leu His Ile Lys Arg Lys Phe
                 25                  30                  35

gag ctg aga tac att cca agt gtg gct act cat gct tca cac cat caa   198
Glu Leu Arg Tyr Ile Pro Ser Val Ala Thr His Ala Ser His His Gln
             40                  45                  50

tcg ttt gac tta aac cag ccc gct gca gag gat gat aat gga gga gac   246
Ser Phe Asp Leu Asn Gln Pro Ala Ala Glu Asp Asp Asn Gly Gly Asp
         55                  60                  65

aac aaa tca ctt ttg tcg aga atg caa aac cca ctt cgt cat ttc agt   294
Asn Lys Ser Leu Leu Ser Arg Met Gln Asn Pro Leu Arg His Phe Ser
     70                  75                  80

gcc tca tct gat tat aat tct tac gaa gat caa ggt tat gtt ctt gat   342
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66 Ala Ser Ser Asp Tyr Asn Ser Tyr Glu Asp Gln Gly Tyr Val Leu Asp
67  85                  90                  95                 100
69 gag gat caa gat tat gct ctt gaa gaa gat gta cca tta ttt ctt gat   390
70 Glu Asp Gln Asp Tyr Ala Leu Glu Glu Asp Val Pro Leu Phe Leu Asp
71                 105                 110                 115
73 gaa gat gta cca tta tta cca agt gtc aag ctt cca att gtt gag aag   438
74 Glu Asp Val Pro Leu Leu Pro Ser Val Lys Leu Pro Ile Val Glu Lys
75             120                 125                 130
77 cta cca cga tcc att aca tgg gtc ttc acc aaa agt agc cag ctg atg   486
78 Leu Pro Arg Ser Ile Thr Trp Val Phe Thr Lys Ser Ser Gln Leu Met
79         135                 140                 145
81 gct gaa agt gat tct gtg att ggt aag aga caa atc tat tat ttg aat   534
82 Ala Glu Ser Asp Ser Val Ile Gly Lys Arg Gln Ile Tyr Tyr Leu Asn
83     150                 155                 160
85 ggt gag gca cta gaa ttg agc agt gaa gaa gat gag gaa gat gaa gaa   582
86 Gly Glu Ala Leu Glu Leu Ser Ser Glu Glu Asp Glu Glu Asp Glu Glu
87 165                 170                 175                 180
89 gaa gat gag gaa gaa atc aag aaa gaa aaa tgc gaa ttt tct gaa gat   630
90 Glu Asp Glu Glu Glu Ile Lys Lys Glu Lys Cys Glu Phe Ser Glu Asp
91                 185                 190                 195
93 gta gac cga ttt ata tgg acg gtt ggg cag gac tat ggt ttg gat gat   678
94 Val Asp Arg Phe Ile Trp Thr Val Gly Gln Asp Tyr Gly Leu Asp Asp
95             200                 205                 210
97 ctg gtc gtg cgg cgt gct ctc gcc aag tac ctc gaa gtg gat gtt tcg   726
98 Leu Val Val Arg Arg Ala Leu Ala Lys Tyr Leu Glu Val Asp Val Ser
99         215                 220                 225
101 gac ata ttg gaa aga tac aat gaa ctc aag ctt aag aat gat gga act   774
102 Asp Ile Leu Glu Arg Tyr Asn Glu Leu Lys Leu Lys Asn Asp Gly Thr
103     230                 235                 240
105 gct ggt gag gct tct gat ttg aca tcc aag aca ata act act gct ttc   822
106 Ala Gly Glu Ala Ser Asp Leu Thr Ser Lys Thr Ile Thr Thr Ala Phe
107 245                 250                 255                 260
109 cag gat ttt gct gat aga cgt cat tgc cgt cgt tgc atg ata ttc gat   870
110 Gln Asp Phe Ala Asp Arg Arg His Cys Arg Arg Cys Met Ile Phe Asp
111                 265                 270                 275
113 tgt cat atg cat gag aag tat gag ccc gag tct aga tcc agc gaa gac   918
114 Cys His Met His Glu Lys Tyr Glu Pro Glu Ser Arg Ser Ser Glu Asp
115             280                 285                 290
117 aaa tct agt ttg ttt gag gat gaa gat aga caa cca tgc agt gag cat   966
118 Lys Ser Ser Leu Phe Glu Asp Glu Asp Arg Gln Pro Cys Ser Glu His
119         295                 300                 305
121 tgt tac ctc aag gtg agg agt gtg aca gaa gct gat cat gtg atg gat  1014
122 Cys Tyr Leu Lys Val Arg Ser Val Thr Glu Ala Asp His Val Met Asp
123     310                 315                 320
125 aat gat aac tct ata tca aac aag att gtg gtc tca gat cca aac aac  1062
126 Asn Asp Asn Ser Ile Ser Asn Lys Ile Val Val Ser Asp Pro Asn Asn
127 325                 330                 335                 340
129 act atg tgg acg cct gta gag aag gat ctt tac ttg aaa gga att gag  1110
130 Thr Met Trp Thr Pro Val Glu Lys Asp Leu Tyr Leu Lys Gly Ile Glu
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133 ata ttt ggg aga aac agt tgt gat gtt gca tta aac ata ctt cgg ggg   1158
134 Ile Phe Gly Arg Asn Ser Cys Asp Val Ala Leu Asn Ile Leu Arg Gly
135             360                 365                 370
137 ctt aag acg tgc cta gag att tac aat tac atg cgc gaa caa gat caa   1206
138 Leu Lys Thr Cys Leu Glu Ile Tyr Asn Tyr Met Arg Glu Gln Asp Gln
139         375                 380                 385
141 tgt act atg tca tta gac ctt aac aaa act aca caa aga cac aat cag   1254
142 Cys Thr Met Ser Leu Asp Leu Asn Lys Thr Thr Gln Arg His Asn Gln
143     390                 395                 400
145 gtt acc aaa aaa gta tct cga aaa agt agt agg tcg gtc cgc aaa aaa   1302
146 Val Thr Lys Lys Val Ser Arg Lys Ser Ser Arg Ser Val Arg Lys Lys
147 405                 410                 415                 420
149 tcg aga ctc cga aaa tat gct cgt tat ccg cct gct tta aag aaa aca   1350
150 Ser Arg Leu Arg Lys Tyr Ala Arg Tyr Pro Pro Ala Leu Lys Lys Thr
151                 425                 430                 435
153 act agt gga gaa gct aag ttt tat aag cac tac aca cca tgc act tgc   1398
154 Thr Ser Gly Glu Ala Lys Phe Tyr Lys His Tyr Thr Pro Cys Thr Cys
155             440                 445                 450
157 aag tca aaa tgt gga cag caa tgc cct tgt tta act cac gaa aat tgc   1446
158 Lys Ser Lys Cys Gly Gln Gln Cys Pro Cys Leu Thr His Glu Asn Cys
159         455                 460                 465
161 tgc gag aaa tat tgc ggg tgc tca aag gat tgc aac aat cgc ttt gga   1494
162 Cys Glu Lys Tyr Cys Gly Cys Ser Lys Asp Cys Asn Asn Arg Phe Gly
163     470                 475                 480
165 gga tgt aat tgt gca att ggc caa tgc aca aat cga caa tgt cct tgt   1542
166 Gly Cys Asn Cys Ala Ile Gly Gln Cys Thr Asn Arg Gln Cys Pro Cys
167 485                 490                 495                 500
169 ttt gct gct aat cgt gaa tgc gat cca gat ctt tgt cgg agt tgt cct   1590
170 Phe Ala Ala Asn Arg Glu Cys Asp Pro Asp Leu Cys Arg Ser Cys Pro
171                 505                 510                 515
173 ctt agc tgt gga gat ggc act ctt ggt gag aca cca gtg caa atc caa   1638
174 Leu Ser Cys Gly Asp Gly Thr Leu Gly Glu Thr Pro Val Gln Ile Gln
175             520                 525                 530
177 tgc aag aac atg caa ttc ctc ctt caa acc aat aaa aag att ctc att   1686
178 Cys Lys Asn Met Gln Phe Leu Leu Gln Thr Asn Lys Lys Ile Leu Ile
179         535                 540                 545
181 gga aag tct gat gtt cat gga tgg ggt gca ttt aca tgg gac tct ctt   1734
182 Gly Lys Ser Asp Val His Gly Trp Gly Ala Phe Thr Trp Asp Ser Leu
183     550                 555                 560
185 aaa aag aat gag tat ctc gga gaa tat act gga gaa ctg atc act cat   1782
186 Lys Lys Asn Glu Tyr Leu Gly Glu Tyr Thr Gly Glu Leu Ile Thr His
187 565                 570                 575                 580
189 gat gaa gct aat gag cgt ggg aga ata gaa gat cgg att ggt tct tcc   1830
190 Asp Glu Ala Asn Glu Arg Gly Arg Ile Glu Asp Arg Ile Gly Ser Ser
191                 585                 590                 595
193 tac ctc ttt acc ttg aat gat cag ctc gaa atc gat gct cgc cgt aaa   1878
194 Tyr Leu Phe Thr Leu Asn Asp Gln Leu Glu Ile Asp Ala Arg Arg Lys
195             600                 605                 610
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197 gga aac gag ttc aaa ttt ctc aat cac tca gca aga cct aac tgc tac   1926
198 Gly Asn Glu Phe Lys Phe Leu Asn His Ser Ala Arg Pro Asn Cys Tyr
199         615                 620                 625
201 gcc aag ttg atg att gtg aga gga gat cag agg att ggt cta ttt gcg   1974
202 Ala Lys Leu Met Ile Val Arg Gly Asp Gln Arg Ile Gly Leu Phe Ala
203     630                 635                 640
205 gag aga gca atc gaa gaa ggt gag gag ctt ttc ttc gac tac tgc tat   2022
206 Glu Arg Ala Ile Glu Glu Gly Glu Glu Leu Phe Phe Asp Tyr Cys Tyr
207 645                 650                 655                 660
209 gga cca gaa cat gcg gat tgg tcg cgt ggt cga gaa cct aga aag act   2070
210 Gly Pro Glu His Ala Asp Trp Ser Arg Gly Arg Glu Pro Arg Lys Thr
211                 665                 670                 675
213 ggt gct tct aaa agg tct aag gaa gcc cgt cca gct cgt tagtttttga   2119
214 Gly Ala Ser Lys Arg Ser Lys Glu Ala Arg Pro Ala Arg
215             680                 685
217 tctgaggaga agcagca                                              2136
220 <210> SEQ ID NO: 2
221 <211> LENGTH: 689
222 <212> TYPE: PRT
223 <213> ORGANISM: Arabidopsis sp.
225 <400> SEQUENCE: 2
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227   1               5                  10                  15
229 Leu Asn Gln Ile Lys Glu Gln Ile Glu Lys Glu Arg Phe Leu His Ile
230             20                  25                  30
232 Lys Arg Lys Phe Glu Leu Arg Tyr Ile Pro Ser Val Ala Thr His Ala
233         35                  40                  45
235 Ser His His Gln Ser Phe Asp Leu Asn Gln Pro Ala Ala Glu Asp Asp
236     50                  55                  60
238 Asn Gly Gly Asp Asn Lys Ser Leu Leu Ser Arg Met Gln Asn Pro Leu
239 65                  70                  75                  80
241 Arg His Phe Ser Ala Ser Ser Asp Tyr Asn Ser Tyr Glu Asp Gln Gly
242                 85                  90                  95
244 Tyr Val Leu Asp Glu Asp Gln Asp Tyr Ala Leu Glu Glu Asp Val Pro
245             100                 105                 110
247 Leu Phe Leu Asp Glu Asp Val Pro Leu Leu Pro Ser Val Lys Leu Pro
248         115                 120                 125
250 Ile Val Glu Lys Leu Pro Arg Ser Ile Thr Trp Val Phe Thr Lys Ser
251     130                 135                 140
253 Ser Gln Leu Met Ala Glu Ser Asp Ser Val Ile Gly Lys Arg Gln Ile
254 145                 150                 155                 160
256 Tyr Tyr Leu Asn Gly Glu Ala Leu Glu Leu Ser Ser Glu Glu Asp Glu
257                 165                 170                 175
259 Glu Asp Glu Glu Glu Asp Glu Glu Glu Ile Lys Lys Glu Lys Cys Glu
260             180                 185                 190
262 Phe Ser Glu Asp Val Asp Arg Phe Ile Trp Thr Val Gly Gln Asp Tyr
263         195                 200                 205
265 Gly Leu Asp Asp Leu Val Val Arg Arg Ala Leu Ala Lys Tyr Leu Glu
266     210                 215                 220
```

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```
268 Val Asp Val Ser Asp Ile Leu Glu Arg Tyr Asn Glu Leu Lys Leu Lys
269 225                 230                 235                 240
271 Asn Asp Gly Thr Ala Gly Glu Ala Ser Asp Leu Thr Ser Lys Thr Ile
272                 245                 250                 255
274 Thr Thr Ala Phe Gln Asp Phe Ala Asp Arg Arg His Cys Arg Arg Cys
275             260                 265                 270
277 Met Ile Phe Asp Cys His Met His Glu Lys Tyr Glu Pro Glu Ser Arg
278         275                 280                 285
280 Ser Ser Glu Asp Lys Ser Ser Leu Phe Glu Asp Glu Asp Arg Gln Pro
281     290                 295                 300
283 Cys Ser Glu His Cys Tyr Leu Lys Val Arg Ser Val Thr Glu Ala Asp
284 305                 310                 315                 320
286 His Val Met Asp Asn Asp Asn Ser Ile Ser Asn Lys Ile Val Val Ser
287                 325                 330                 335
289 Asp Pro Asn Asn Thr Met Trp Thr Pro Val Glu Lys Asp Leu Tyr Leu
290             340                 345                 350
292 Lys Gly Ile Glu Ile Phe Gly Arg Asn Ser Cys Asp Val Ala Leu Asn
293         355                 360                 365
295 Ile Leu Arg Gly Leu Lys Thr Cys Leu Glu Ile Tyr Asn Tyr Met Arg
296     370                 375                 380
298 Glu Gln Asp Gln Cys Thr Met Ser Leu Asp Leu Asn Lys Thr Thr Gln
299 385                 390                 395                 400
301 Arg His Asn Gln Val Thr Lys Lys Val Ser Arg Lys Ser Ser Arg Ser
302                 405                 410                 415
304 Val Arg Lys Lys Ser Arg Leu Arg Lys Tyr Ala Arg Tyr Pro Pro Ala
305             420                 425                 430
307 Leu Lys Lys Thr Thr Ser Gly Glu Ala Lys Phe Tyr Lys His Tyr Thr
308         435                 440                 445
310 Pro Cys Thr Cys Lys Ser Lys Cys Gly Gln Gln Cys Pro Cys Leu Thr
311     450                 455                 460
313 His Glu Asn Cys Cys Glu Lys Tyr Cys Gly Cys Ser Lys Asp Cys Asn
314 465                 470                 475                 480
316 Asn Arg Phe Gly Gly Cys Asn Cys Ala Ile Gly Gln Cys Thr Asn Arg
317                 485                 490                 495
319 Gln Cys Pro Cys Phe Ala Ala Asn Arg Glu Cys Asp Pro Asp Leu Cys
320             500                 505                 510
322 Arg Ser Cys Pro Leu Ser Cys Gly Asp Gly Thr Leu Gly Glu Thr Pro
323         515                 520                 525
325 Val Gln Ile Gln Cys Lys Asn Met Gln Phe Leu Leu Gln Thr Asn Lys
326     530                 535                 540
328 Lys Ile Leu Ile Gly Lys Ser Asp Val His Gly Trp Gly Ala Phe Thr
329 545                 550                 555                 560
331 Trp Asp Ser Leu Lys Lys Asn Glu Tyr Leu Gly Glu Tyr Thr Gly Glu
332                 565                 570                 575
334 Leu Ile Thr His Asp Glu Ala Asn Glu Arg Gly Arg Ile Glu Asp Arg
335             580                 585                 590
337 Ile Gly Ser Ser Tyr Leu Phe Thr Leu Asn Asp Gln Leu Glu Ile Asp
338         595                 600                 605
340 Ala Arg Arg Lys Gly Asn Glu Phe Lys Phe Leu Asn His Ser Ala Arg
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VERIFICATION SUMMARY DATE: 07/30/2001
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Input Set : **N:\Crf3\RULE60\09812283.txt**
Output Set: **N:\CRF3\07302001\I812283.raw**

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L:821 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
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L:845 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
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Input Set : N:\Crf3\RULE60\09812283.txt
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